

LOCUS AF089816 **1765 bp** **mRNA linear** PRI 24-OCT-1998
DEFINITION Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.
ACCESSION AF089816
VERSION AF089816.1 GI:3789933
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1765)
AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.
TITLE GIPC, a PDZ domain containing protein, interacts specifically with
the C terminus of RGS-GAIP
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12340-12345 (1998)
MEDLINE 98445373
PUBMED 9770488
REFERENCE 2 (bases 1 to 1765)
AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1998) CMM, UCSD, 9500 Gilman Drive, La Jolla, CA
92093, USA
FEATURES Location/Qualifiers
source
1. .1765
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/note="growth hormone secreting cells"
CDS
88. .1089
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/db_xref="GI:3789934"
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MGLPPPPPALARPRLVFHTQLAHGSPTGRIEGFTNVKELYGKIAEAFLPTAEVMFCTL
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KEGSVIDHIHLISVGDMIEAINQSQLLGCRHYEVARLLKELPRGRTFTLKLTEPRKAF
DMISQRSAGGRPGSGPQLGTGRGTLRLRSRGPATVEDLPSAFEEKAIKEVDDLESYM
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/note="encodes PDZ domain"
misc_feature 877. .1047
/note="encodes ACP domain"
BASE COUNT 332 a 561 c 568 g 304 t
ORIGIN
Alignment Scores:
Pred. No.: 2.08e-102 Length: 1765
Score: 1713.00 Matches: 330
Percent Similarity: 99.10% Conservative: 0
Best Local Similarity: 99.10% Mismatches: 3
Query Match: 99.59% Indels: 0
DB: 9 Gaps: 0

US-10-013-056-2 (1-333) x AF089816 (1-1765)

Qy	1	MetProLeuGlyLeuGlyArgArgLysLysAlaProProLeuValGluAsnGluGluAla	20
Db	88	ATGCCGCTGGACTGGGCAGCCGGAAAAAGGCGCCCCCTCTAGTGGAAAATGAGGAGGCT	147
Qy	21	GluProGlyArgGlyGlyLeuGlyValGlyGluProGlyProLeuGlyGlyGlySer	40
Db	148	GAGCCAGGCCGTGGAGGGCTGGCGTGGGGAGCCAGGGCCTTGGCCGGAGGTGGTCG	207
Qy	41	Gly***ProGlnMetGly*****ProProProProAlaLeuArgProArgLeuValPhe	60
Db	208	GGGGGCCCAAAATGGGCTTGCCCCCCCCTCCCCAGCCCTGCGGCCCGCCTGTGTT	267
Qy	61	HisThrGlnLeuAlaHisGlySerProThrGlyArgIleGluGlyPheThrAsnValLys	80
Db	268	CACACCCAGCTGGCCATGGCAGTCCCCTGGCCGCATCGAGGGGTTCACCAACGTCAAG	327
Qy	81	GluLeuTyrGlyLysIleAlaGluAlaPheArgLeuProThrAlaGluValMetPheCys	100
Db	328	GAGCTGTATGGCAAGATTGCCGAGGCCTTCCGCCTGCCACTGCCGAGGTGATGTTTG	387
Qy	101	ThrLeuAsnThrHisLysValAspMetAspLysLeuLeuGlyGlyGlnIleGlyLeuGlu	120
Db	388	ACCCTGAACACCCACAAAGTGGACATGGACAAGCTCCTGGGGGCCAATCGGCTGGAG	447
Qy	121	AspPheIlePheAlaHisValLysGlyGlnArgLysGluValGluValPheLysSerGlu	140
Db	448	GACTTCATCTCGCCCACGTGAAGGGCAGCGCAAGGAGGTGGAGGTGTTCAAGTCGGAG	507
Qy	141	AspAlaLeuGlyLeuThrIleThrAspAsnGlyAlaGlyTyrAlaPheIleLysArgIle	160
Db	508	GATGCACTCGGGCTCACCATCACGGACAACGGGGCTGGTACGCCCTCATCAAGCGCATC	567
Qy	161	LysGluGlySerValIleAspHisIleHisLeuIleSerValGlyAspMetIleGluAla	180
Db	568	AAGGAGGGCAGCGTGATCGACCACATCCACCTCATCAGCGTGGCGACATGATCGAGGCC	627
Qy	181	IleAsnGlyGlnSerLeuLeuGlyCysArgHisTyrGluValAlaArgLeuLeuLysGlu	200
Db	628	ATTAACGGGCAGAGCCTGCTGGCTGCCGGACTACGAAGTGGCCGGCTGCTCAAGGAA	687
Qy	201	LeuProArgGlyArgThrPheThrLeuLysLeuThrGluProArgLysAlaPheAspMet	220
Db	688	CTGCCCGAGGCCGTACCTCACGCTGAAGCTCACGGAGCCTCGCAAGGCCCTCGACATG	747
Qy	221	IleSerGlnArgSerAlaGlyGlyArgProGlySerGlyProGlnLeuGlyThrGlyArg	240
Db	748	ATCAGCCAGCGTTCAGCGGGTGGCCGCCCTGGCTCTGGCCCACAACTGGGCACTGGCCGA	807
Qy	241	GlyThrLeuArgLeuArgSerArgGlyProAlaThrValGluAspLeuProSerAlaPhe	260
Db	808	GGGACCCCTGCGGCTCCGATCCCAGGGCCACGGTGGAGGATCTGCCCTCGCCTTT	867
Qy	261	GluGluLysAlaIleGluLysValAspAspLeuLeuGluSerTyrMetGlyIleArgAsp	280
Db	868	GAAGAGAAGGCCATTGAGAAGGTGGATGACCTGCTGGAGAGTTACATGGGTATCAGGGAC	927
Qy	281	ThrGluLeuAlaAlaThrMetValGluLeuGlyLysAspLysArgAsnProAspGluLeu	300

Db 928 ACGGAGCTGGCGGCCACCATGGTGGAGCTGGGAAAGGACAAAAGGAACCCGGATGAGCTG 987
Qy 301 AlaGluAlaLeuAspGluArgLeuGlyAspPheAlaPheProAspGluPheValPheAsp 320
Db 988 GCCGAGGCCCTGGACGAACGGCTGGGTGACTTGCCTCCCTGACGAGTTCGTCTTGAC 1047
Qy 321 ValTrpGlyAlaIleGlyAspAlaLysValGlyArgTyr 333
Db 1048 GTCTGGGGCGCCATTGGGGACGCCAAGGTCGGCCGCTAC 1086